

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:14:08 ; Search time 190 Seconds
 (without alignments)
 1782.953 Million cell updates/sec

Title: US-10-067-632-54
 Perfect score: 4201
 Sequence: 1 MGWLTRIVCLFWGVLLTARA.....ENKKGRNRRTHEFERAPRSV 771

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	4201	100.0	771	2	AAR71380	Aar71380	Human sem
2	4201	100.0	771	4	AAG62726	Aag62726	Amino aci
3	4201	100.0	771	5	ABG96413	Abg96413	Human ova
4	4201	100.0	771	7	ADD08934	Add08934	Human sem
5	4201	100.0	771	7	ADE25760	Ade25760	Human pro
6	4201	100.0	771	8	ADQ19751	Adq19751	Human sof
7	4201	100.0	771	9	ADZ00426	Adz00426	Semaphori
8	4197	99.9	770	7	ADN95333	Adn95333	Human BEC

9	4181	99.5	796	2	AAy21264	Aay21264	Human	sem
10	2562	61.0	477	2	AAR74175	Aar74175	Human	col
11	2245.5	53.5	777	2	AAy27127	Aay27127	Human	bra
12	2245.5	53.5	777	3	AAy99427	Aay99427	Human	PRO
13	2245.5	53.5	777	4	AAB66176	Aab66176	Protein	o
14	2245.5	53.5	777	4	AAU29197	Aau29197	Human	PRO
15	2245.5	53.5	777	6	ABU58573	Abu58573	Human	PRO
16	2245.5	53.5	777	6	ABU88121	Abu88121	Novel	hum
17	2245.5	53.5	777	6	ABU84436	Abu84436	Human	sec
18	2245.5	53.5	777	6	ABR66310	Abr66310	Human	sec
19	2245.5	53.5	777	6	ABR65700	Abr65700	Human	sec
20	2245.5	53.5	777	6	ABU99640	Abu99640	Human	sec
21	2245.5	53.5	777	6	ABU82879	Abu82879	Human	PRO
22	2245.5	53.5	777	6	ABU90000	Abu90000	Novel	hum
23	2245.5	53.5	777	6	ABR68249	Abr68249	Human	sec
24	2245.5	53.5	777	6	ABU96302	Abu96302	Novel	hum
25	2245.5	53.5	777	6	ABU92733	Abu92733	Human	sec
26	2245.5	53.5	777	6	ABO08810	Abo08810	Human	sec
27	2245.5	53.5	777	6	ABO02862	Abo02862	Human	sec
28	2245.5	53.5	777	6	ABR75016	Abr75016	Human	sec
29	2245.5	53.5	777	6	ABR94778	Abr94778	Human	sec
30	2245.5	53.5	777	6	ABU85751	Abu85751	Human	PRO
31	2245.5	53.5	777	6	ABU98911	Abu98911	Novel	hum
32	2245.5	53.5	777	6	ABU98126	Abu98126	Novel	hum
33	2245.5	53.5	777	6	ABU91832	Abu91832	Novel	hum
34	2245.5	53.5	777	6	ABU89525	Abu89525	Human	PRO
35	2245.5	53.5	777	6	ABU86366	Abu86366	Human	sec
36	2245.5	53.5	777	6	ABU67579	Abu67579	Human	sec
37	2245.5	53.5	777	6	ABU80607	Abu80607	Human	PRO
38	2245.5	53.5	777	6	ABR99525	Abr99525	Human	sec
39	2245.5	53.5	777	6	ABR98915	Abr98915	Human	sec
40	2245.5	53.5	777	6	ABO16438	Abo16438	Human	sec
41	2245.5	53.5	777	6	ABR92338	Abr92338	Human	sec
42	2245.5	53.5	777	6	ABO18979	Abo18979	Human	sec
43	2245.5	53.5	777	6	ABR78400	Abr78400	Human	sec
44	2245.5	53.5	777	6	ABU85136	Abu85136	Novel	hum
45	2245.5	53.5	777	6	ABO00275	Abo00275	Novel	hum

ALIGNMENTS

RESULT 1

AAR71380

ID AAR71380 standard; protein; 771 AA.

XX

AC AAR71380;

XX

DT 25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

XX

DE Human semaphorin III protein.

XX

KW Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium;

KW variola major virus; smallpox; semaphorin receptor binding activity;

KW modulation; nerve cell growth; immune response; viral pathogenesis;

KW neurological disease; neuro-regeneration; oncological infection.

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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:15:20 ; Search time 30 Seconds
(without alignments)
2124.765 Million cell updates/sec

Title: US-10-067-632-54
Perfect score: 4201
Sequence: 1 MGWLTRIVCLFWGVLLTARA.....ENKKGRNRRTHEFERAPRSV 771

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4201	100.0	771	1	US-08-121-713D-54	Sequence 54, Appl
2	4201	100.0	771	1	US-08-835-268-54	Sequence 54, Appl
3	4201	100.0	771	1	US-09-060-692-54	Sequence 54, Appl
4	4201	100.0	771	2	US-08-833-391-54	Sequence 54, Appl
5	4201	100.0	771	2	US-09-060-610-54	Sequence 54, Appl
6	4201	100.0	771	4	PCT-US94-10151A-54	Sequence 54, Appl
7	3568	84.9	655	2	US-08-556-422A-3	Sequence 3, Appli
8	2562	61.0	477	1	US-08-136-922-2	Sequence 2, Appli
9	2245.5	53.5	777	2	US-10-012-231A-310	Sequence 310, App
10	2245.5	53.5	777	2	US-10-015-389A-310	Sequence 310, App
11	2245.5	53.5	777	2	US-10-006-768A-310	Sequence 310, App

12	2245.5	53.5	777	2	US-10-015-671A-310	Sequence 310, App
13	2245.5	53.5	777	2	US-10-015-393A-310	Sequence 310, App
14	2245.5	53.5	777	2	US-10-011-833A-310	Sequence 310, App
15	2245.5	53.5	777	2	US-10-006-041A-310	Sequence 310, App
16	2245.5	53.5	777	2	US-10-012-064A-310	Sequence 310, App
17	2030	48.3	775	2	US-09-308-179B-1	Sequence 1, Appli
18	1830	43.6	782	2	US-09-813-290-4	Sequence 4, Appli
19	1830	43.6	875	2	US-09-813-290-2	Sequence 2, Appli
20	1042.5	24.8	433	2	US-09-964-956-77	Sequence 77, Appl
21	982.5	23.4	862	2	US-08-556-422A-2	Sequence 2, Appli
22	966	23.0	834	2	US-10-188-495-65	Sequence 65, Appl
23	957	22.8	430	2	US-09-964-956-76	Sequence 76, Appl
24	937	22.3	838	2	US-09-854-845-29	Sequence 29, Appl
25	937	22.3	865	2	US-09-854-845-33	Sequence 33, Appl
26	927.5	22.1	843	2	US-09-854-845-27	Sequence 27, Appl
27	927.5	22.1	870	2	US-09-854-845-31	Sequence 31, Appl
28	891	21.2	697	2	US-09-854-845-25	Sequence 25, Appl
29	888	21.1	837	2	US-10-012-231A-253	Sequence 253, App
30	888	21.1	837	2	US-10-015-389A-253	Sequence 253, App
31	888	21.1	837	2	US-10-006-768A-253	Sequence 253, App
32	888	21.1	837	2	US-10-015-671A-253	Sequence 253, App
33	888	21.1	837	2	US-10-015-393A-253	Sequence 253, App
34	888	21.1	837	2	US-10-011-833A-253	Sequence 253, App
35	888	21.1	837	2	US-10-006-041A-253	Sequence 253, App
36	888	21.1	837	2	US-10-012-064A-253	Sequence 253, App
37	881.5	21.0	702	2	US-09-854-845-23	Sequence 23, Appl
38	854.5	20.3	739	2	US-09-854-845-45	Sequence 45, Appl
39	854.5	20.3	766	2	US-09-854-845-49	Sequence 49, Appl
40	854.5	20.3	939	2	US-09-520-781-4	Sequence 4, Appli
41	854.5	20.3	939	2	US-09-957-187-4	Sequence 4, Appli
42	854.5	20.3	939	2	US-09-991-053-4	Sequence 4, Appli
43	854	20.3	1047	2	US-09-957-187-85	Sequence 85, Appl
44	852.5	20.3	626	2	US-09-957-187-83	Sequence 83, Appl
45	852.5	20.3	630	2	US-09-520-781-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-08-121-713D-54

; Sequence 54, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:15:52 ; Search time 62 Seconds
(without alignments)
5195.910 Million cell updates/sec

Title: US-10-067-632-54
Perfect score: 4201
Sequence: 1 MGWLTRIVCLFWGVLLTARA.....ENKKGRNRRTHEFERAPRSV 771

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4201	100.0	771	4	US-10-097-340-284	Sequence 284, App
2	4201	100.0	771	4	US-10-262-538-10	Sequence 10, Appl
3	4201	100.0	771	4	US-10-067-632-54	Sequence 54, Appl
4	4201	100.0	771	4	US-10-247-671-164	Sequence 164, App
5	4201	100.0	771	4	US-10-669-176-10	Sequence 10, Appl
6	4201	100.0	771	5	US-10-723-860-2570	Sequence 2570, Ap
7	4201	100.0	771	6	US-11-050-926-284	Sequence 284, App
8	3568	84.9	655	4	US-10-320-769-3	Sequence 3, Appli
9	2245.5	53.5	777	3	US-09-946-374-310	Sequence 310, App
10	2245.5	53.5	777	4	US-10-052-586-348	Sequence 348, App
11	2245.5	53.5	777	4	US-10-174-590-348	Sequence 348, App

12	2245.5	53.5	777	4	US-10-176-758-348	Sequence 348, App
13	2245.5	53.5	777	4	US-10-175-737-348	Sequence 348, App
14	2245.5	53.5	777	4	US-10-174-581-348	Sequence 348, App
15	2245.5	53.5	777	4	US-10-176-483-348	Sequence 348, App
16	2245.5	53.5	777	4	US-10-176-749-348	Sequence 348, App
17	2245.5	53.5	777	4	US-10-176-914-348	Sequence 348, App
18	2245.5	53.5	777	4	US-10-176-915-348	Sequence 348, App
19	2245.5	53.5	777	4	US-10-173-706-348	Sequence 348, App
20	2245.5	53.5	777	4	US-10-175-738-348	Sequence 348, App
21	2245.5	53.5	777	4	US-10-175-752-348	Sequence 348, App
22	2245.5	53.5	777	4	US-10-176-482-348	Sequence 348, App
23	2245.5	53.5	777	4	US-10-176-757-348	Sequence 348, App
24	2245.5	53.5	777	4	US-10-176-913-348	Sequence 348, App
25	2245.5	53.5	777	4	US-10-180-552-348	Sequence 348, App
26	2245.5	53.5	777	4	US-10-180-557-348	Sequence 348, App
27	2245.5	53.5	777	4	US-10-173-700-348	Sequence 348, App
28	2245.5	53.5	777	4	US-10-174-572-348	Sequence 348, App
29	2245.5	53.5	777	4	US-10-174-579-348	Sequence 348, App
30	2245.5	53.5	777	4	US-10-174-582-348	Sequence 348, App
31	2245.5	53.5	777	4	US-10-174-588-348	Sequence 348, App
32	2245.5	53.5	777	4	US-10-175-739-348	Sequence 348, App
33	2245.5	53.5	777	4	US-10-175-740-348	Sequence 348, App
34	2245.5	53.5	777	4	US-10-175-743-348	Sequence 348, App
35	2245.5	53.5	777	4	US-10-176-488-348	Sequence 348, App
36	2245.5	53.5	777	4	US-10-176-492-348	Sequence 348, App
37	2245.5	53.5	777	4	US-10-176-747-348	Sequence 348, App
38	2245.5	53.5	777	4	US-10-176-750-348	Sequence 348, App
39	2245.5	53.5	777	4	US-10-176-985-348	Sequence 348, App
40	2245.5	53.5	777	4	US-10-176-987-348	Sequence 348, App
41	2245.5	53.5	777	4	US-10-176-992-348	Sequence 348, App
42	2245.5	53.5	777	4	US-10-176-993-348	Sequence 348, App
43	2245.5	53.5	777	4	US-10-184-658-348	Sequence 348, App
44	2245.5	53.5	777	4	US-10-176-991-348	Sequence 348, App
45	2245.5	53.5	777	4	US-10-173-695-348	Sequence 348, App

ALIGNMENTS

RESULT 1

US-10-097-340-284

; Sequence 284, Application US/10097340

; Publication No. US20030087250A1

; GENERAL INFORMATION:

; APPLICANT: John MONAHAN

; APPLICANT: Manjula GANNAVARAPU

; APPLICANT: Sebastian HOERSCH

; APPLICANT: Shubhangi KAMATKAR

; APPLICANT: Steve G. KOVATS

; APPLICANT: Rachel E. MEYERS

; APPLICANT: Michael MORRISEY

; APPLICANT: Peter OLANDT

; APPLICANT: Ami SEN

; APPLICANT: Peter VEIBY

; APPLICANT: Gordon B. MILLS

; APPLICANT: Robert C. BAST, Jr.

; APPLICANT: Karen LU

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:16:11 ; Search time 17 Seconds
 (without alignments)
 1414.648 Million cell updates/sec

Title: US-10-067-632-54
 Perfect score: 4201
 Sequence: 1 MGWLTRIVCLFWGVLLTARA.....ENKKGRNRRTHEFERAPRSV 771

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:*
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 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2587	61.6	489	7	US-11-124-607-12	Sequence 12, Appl
2	2106.5	50.1	748	6	US-10-821-234-1479	Sequence 1479, Ap
3	1042.5	24.8	433	6	US-10-877-346-77	Sequence 77, Appl
4	957	22.8	430	6	US-10-877-346-76	Sequence 76, Appl
5	845.5	20.1	975	6	US-10-745-586-161	Sequence 161, App
6	818	19.5	477	7	US-11-124-607-11	Sequence 11, Appl
7	752.5	17.9	776	6	US-10-925-970-3	Sequence 3, Appli
8	722.5	17.2	1074	6	US-10-501-035-311	Sequence 311, App
9	712.5	17.0	888	6	US-10-131-826A-544	Sequence 544, App

10	712.5	17.0	888	6	US-10-973-115B-544	Sequence 544, App
11	654.5	15.6	666	6	US-10-933-746-3	Sequence 3, Appli
12	647	15.4	629	7	US-11-072-512-2289	Sequence 2289, Ap
13	536.5	12.8	587	6	US-10-925-970-6	Sequence 6, Appli
14	382	9.1	245	6	US-10-453-195-12	Sequence 12, Appl
15	363	8.6	394	6	US-10-933-746-4	Sequence 4, Appli
16	256	6.1	132	7	US-11-072-512-2890	Sequence 2890, Ap
17	200	4.8	1896	6	US-10-877-346-13	Sequence 13, Appl
18	180.5	4.3	1871	6	US-10-877-346-42	Sequence 42, Appl
19	172	4.1	1963	6	US-10-877-346-43	Sequence 43, Appl
20	170	4.0	1905	6	US-10-877-346-44	Sequence 44, Appl
21	119.5	2.8	1985	6	US-10-501-035-218	Sequence 218, App
22	115.5	2.7	1382	7	US-11-208-414-7	Sequence 7, Appli
23	114.5	2.7	1382	7	US-11-208-414-9	Sequence 9, Appli
24	114	2.7	1479	6	US-10-204-639-4	Sequence 4, Appli
25	100	2.4	520	6	US-10-467-657-1992	Sequence 1992, Ap
26	100	2.4	701	7	US-11-189-301-19	Sequence 19, Appl
27	100	2.4	766	7	US-11-189-301-21	Sequence 21, Appl
28	100	2.4	927	7	US-11-189-301-10	Sequence 10, Appl
29	100	2.4	3623	6	US-10-995-561-593	Sequence 593, App
30	99.5	2.4	1767	7	US-11-052-554A-372	Sequence 372, App
31	99.5	2.4	1767	7	US-11-089-508-4	Sequence 4, Appli
32	98.5	2.3	355	7	US-11-096-568A-11146	Sequence 11146, A
33	98.5	2.3	8746	7	US-11-098-686-10232	Sequence 10232, A
34	98	2.3	497	6	US-10-793-626-1624	Sequence 1624, Ap
35	98	2.3	954	7	US-11-096-568A-31293	Sequence 31293, A
36	98	2.3	963	7	US-11-096-568A-31292	Sequence 31292, A
37	98	2.3	964	7	US-11-096-568A-31291	Sequence 31291, A
38	96	2.3	1076	7	US-11-098-686-11338	Sequence 11338, A
39	96	2.3	2204	6	US-10-495-083-8	Sequence 8, Appli
40	95.5	2.3	1154	6	US-10-330-773-867	Sequence 867, App
41	95.5	2.3	1390	6	US-10-957-351-1	Sequence 1, Appli
42	95.5	2.3	1390	7	US-11-124-607-2	Sequence 2, Appli
43	95	2.3	484	6	US-10-873-528-38	Sequence 38, Appl
44	93.5	2.2	749	6	US-10-481-935A-105	Sequence 105, App
45	93.5	2.2	1009	6	US-10-912-971-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-11-124-607-12

; Sequence 12, Application US/11124607

; Publication No. US20060069019A1

; GENERAL INFORMATION:

; APPLICANT: Wiesmann, Christopher

; APPLICANT: Stamos, Jennifer

; TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE COMPLEX OF HEPATOCYTE GROWTH FACTOR BETA

; TITLE OF INVENTION: CHAIN WITH MET RECEPTOR AND METHODS OF USE

; FILE REFERENCE: 11669.178USU1

; CURRENT APPLICATION NUMBER: US/11/124,607

; CURRENT FILING DATE: 2005-05-06

; PRIOR APPLICATION NUMBER: US 60/568,865

; PRIOR FILING DATE: 2004-05-06

; NUMBER OF SEQ ID NOS: 14

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:15:02 ; Search time 27 Seconds
 (without alignments)
 2747.523 Million cell updates/sec

Title: US-10-067-632-54
 Perfect score: 4201
 Sequence: 1 MGWLTRIVCLFWGVLLTARA.....ENKKGRNRRTHEFERAPRSV 771

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4201	100.0	771	2	D49423	semaphorin III pre
2	3989.5	95.0	772	2	I48747	semaphorin D - mou
3	3784.5	90.1	772	2	A49069	collapsin - chicke
4	3478.5	82.8	666	2	I58169	semaphorin III - m
5	2118	50.4	749	2	G01856	semaphorin V - hum
6	2059.5	49.0	748	2	I48744	semaphorin A - mou
7	1952	46.5	753	2	G02173	semaphorin III fam
8	1850.5	44.0	751	2	I48748	semaphorin E - mou
9	966	23.0	834	2	S66498	M-sema F protein p
10	857.5	20.4	782	2	I48746	semaphorin C - mou
11	828	19.7	1011	2	JC8059	semaphorin 6D-1 -
12	802	19.1	760	2	I48745	semaphorin B - mou
13	783.5	18.7	724	2	C49423	semaphorin II prec

14	766.5	18.2	730	2	JH0798	fasciclin IV precu
15	731.5	17.4	656	2	B49423	semaphorin I - fru
16	722.5	17.2	1074	2	JC5928	semaphorin F precu
17	685	16.3	712	2	T27165	hypothetical prote
18	678	16.1	711	2	A49423	semaphorin I precu
19	530	12.6	653	2	T03102	semaphorin homolog
20	327	7.8	676	2	T33853	hypothetical prote
21	195	4.6	1894	2	JC4980	plexin 1 precursor
22	188.5	4.5	1945	2	T13937	plexin A - fruit f
23	186	4.4	1872	2	JC4976	plexin 3 precursor
24	184	4.4	441	2	S29921	hypothetical prote
25	180	4.3	403	2	E42521	A39R protein - vac
26	172	4.1	1884	2	JC4975	plexin 2 precursor
27	170	4.0	1905	2	I51553	Plexin - African c
28	167	4.0	2051	2	T13164	plexin B - fruit f
29	154.5	3.7	1568	2	T09074	semaphorin recepto
30	134.5	3.2	1806	2	T23298	hypothetical prote
31	127.5	3.0	295	2	JQ1775	SalL9R protein - v
32	123	2.9	573	1	CSBYT	catalase (EC 1.11.
33	117.5	2.8	1379	1	S01254	hepatocyte growth
34	115.5	2.7	904	2	S53896	DNA mismatch repai
35	112.5	2.7	248	2	A46652	glucosamine-6-phos
36	111.5	2.7	1104	1	A36866	microbial collagen
37	110	2.6	3078	2	T28432	variant-specific s
38	109.5	2.6	613	2	T19677	hypothetical prote
39	109.5	2.6	766	2	S37894	hypothetical prote
40	109.5	2.6	1664	2	T18216	integrin-like prot
41	108	2.6	1276	2	T09204	probable tail-host
42	108	2.6	1291	2	T09273	probable tail-host
43	108	2.6	1375	2	T30813	plasminogen relate
44	108	2.6	1654	2	AI2067	two-component sens
45	106.5	2.5	1240	2	T03097	CDO protein - huma

ALIGNMENTS

RESULT 1

D49423

semaphorin III precursor - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: D49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: "The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: D49423

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-771 <KOL>

A;Cross-references: UNIPROT:Q14563; UNIPARC:UPI0000135A60; GB:L26081;

NID:g799328; PIDN:AAA65938.1; PID:g436560

C;Genetics:

A;Gene: GDB:SEMA1

A;Cross-references: GDB:283448

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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:14:33 ; Search time 235 Seconds
 (without alignments)
 2314.733 Million cell updates/sec

Title: US-10-067-632-54
 Perfect score: 4201
 Sequence: 1 MGWLTRIVCLFWGVLLTARA.....ENKKGRNRRTHEFERAPRSV 771

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%				
No.	Score	Query	Match	Length	ID	Description
1	4201	100.0	771	1	SEM3A_HUMAN	Q14563 homo sapien
2	4057.5	96.6	772	1	SEM3A_RAT	Q63548 rattus norv
3	4035.5	96.1	772	1	SEM3A_MOUSE	O08665 mus musculu
4	4035.5	96.1	772	2	Q5BL08_MOUSE	Q5bl08 mus musculu
5	3784.5	90.1	772	1	SEM3A_CHICK	Q90607 gallus gall
6	3609.5	85.9	774	2	Q8JIW9_XENLA	Q8jiw9 xenopus lae
7	3207.5	76.4	778	1	SE3AB_BRARE	Q9w686 brachydanio
8	3075.5	73.2	860	1	SE3AA_BRARE	Q9w7j1 brachydanio
9	2947	70.1	870	2	Q4SBS9_TETNG	Q4sbs9 tetraodon n
10	2257.5	53.7	777	2	Q8BH34_MOUSE	Q8bh34 m mus muscu
11	2251.5	53.6	777	2	Q8BMF6_MOUSE	Q8bmf6 mus musculu
12	2247.5	53.5	777	1	SEM3D_HUMAN	O95025 homo sapien
13	2242.5	53.4	761	1	SEM3D_CHICK	Q90663 gallus gall
14	2163	51.5	710	2	Q4T175_TETNG	Q4t175 tetraodon n
15	2125	50.6	764	1	SEM3D_BRARE	Q9w6g6 brachydanio

16	2118	50.4	749	1	SEM3B_HUMAN	Q13214	homo sapien
17	2106.5	50.1	748	2	Q6GU46_HUMAN	Q6gu46	homo sapien
18	2059.5	49.0	748	1	SEM3B_MOUSE	Q62177	mus musculu
19	2044	48.7	775	1	SEM3E_HUMAN	O15041	homo sapien
20	2037	48.5	725	2	Q4REZ9_TETNG	Q4rez9	tetraodon n
21	2030	48.3	775	2	Q9QX23_MOUSE	Q9qx23	mus musculu
22	2020	48.1	775	1	SEM3E_MOUSE	P70275	mus musculu
23	2008.5	47.8	685	2	Q66KH4_XENLA	Q66kh4	xenopus lae
24	2005.5	47.7	756	2	Q8QGU9_CHICK	Q8qgu9	gallus gall
25	1993	47.4	785	1	SEM3E_CHICK	O42237	gallus gall
26	1957	46.6	750	2	Q59G50_HUMAN	Q59g50	homo sapien
27	1955	46.5	747	2	Q4SR41_TETNG	Q4sr41	tetraodon n
28	1940	46.2	785	1	SEM3F_HUMAN	Q13275	homo sapien
29	1938	46.1	785	2	Q6GTR4_HUMAN	Q6gtr4	homo sapien
30	1937.5	46.1	796	2	Q5ID24_BRARE	Q5id24	brachydanio
31	1928	45.9	785	1	SEM3F_MOUSE	O88632	mus musculu
32	1916.5	45.6	743	2	Q5ID23_BRARE	Q5id23	brachydanio
33	1905.5	45.4	772	2	Q4RXA8_TETNG	Q4rxa8	tetraodon n
34	1894	45.1	751	1	SEM3C_CHICK	O42236	gallus gall
35	1883.5	44.8	398	2	Q4U3E4_9PASS	Q4u3e4	lonchura st
36	1862.5	44.3	751	2	Q6NXW7_MOUSE	Q6nxw7	mus musculu
37	1861	44.3	640	2	Q5U4Y0_XENTR	Q5u4y0	xenopus tro
38	1850.5	44.0	751	1	SEM3C_MOUSE	Q62181	mus musculu
39	1849.5	44.0	751	1	SEM3C_HUMAN	Q99985	homo sapien
40	1848.5	44.0	751	2	Q5RE75_PONPY	Q5re75	pongo pygma
41	1844	43.9	745	2	Q5ID21_BRARE	Q5id21	brachydanio
42	1830.5	43.6	780	2	Q4LFA9_MOUSE	Q4lfa9	mus musculu
43	1830	43.6	782	2	Q9NS98_HUMAN	Q9ns98	homo sapien
44	1824.5	43.4	748	2	Q5XGY3_XENLA	Q5xgy3	xenopus lae
45	1808	43.0	712	2	Q5RGH9_BRARE	Q5rgh9	brachydanio

ALIGNMENTS

RESULT 1

SEM3A_HUMAN

ID SEM3A_HUMAN STANDARD; PRT; 771 AA.
 AC Q14563;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III).
 GN Name=SEMA3A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fetal brain;
 RX MEDLINE=94094332; PubMed=8269517;
 RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
 RT "The semaphorin genes encode a family of transmembrane and secreted
 growth cone guidance molecules.";
 RL Cell 75:1389-1399(1993).